Amendments To The Claims

1. (Currently Amended) A method of identifying bacteria, comprising:
   a) providing:
      i) amplified random genomic DNA sequences from a plurality of bacterial reference species, wherein said amplified genomic sequences range between 1 – 2 kb and are arrayed on a solid support ~~so as to create a plurality of arrayed elements~~, and wherein ~~the nucleotide sequence of~~ said amplified genomic DNA sequences comprise[[s]] unknown sequences,
      ii) labeled target DNA from a test bacteria of interest, wherein said labeled target DNA is labeled with a first fluorescent dye, and
      iii) labeled reference DNA from at least four ~~strains~~ of said bacterial reference species ~~bacteria, wherein said reference bacteria are members of the group consisting of said plurality of bacterial species,~~ wherein said labeled reference DNA is labeled with a second fluorescent dye,
   b) hybridizing said target DNA and said reference DNA to said amplified genomic DNA sequences ~~having unknown sequences on said plurality of arrayed elements~~, wherein each hybridized target DNA has a fluorescent target DNA signal, and each hybridized reference DNA has a fluorescent reference DNA signal,
   c) ~~determining the presence of 70% homology between said hybridized target DNA and one or more of said reference DNA by~~ comparing said fluorescent target DNA signal with said fluorescent reference DNA signal, and
   d) identifying~~, without the need for sequencing said amplified genomic sequences,~~ the species of said test bacteria ~~based on said homology~~.

2. (Original) The method of claim 1, wherein said test bacteria are from a sample obtained from a subject.

3. (Previously Presented) The method of claim 1, wherein said test bacteria are pathogenic.

4. (Original) The method of claim 1, wherein said test bacteria are environmental isolates.

5. (Original) The method of claim 1, wherein said solid support is a microchip.

6. (Previously Presented) The method of claim 26, wherein said calculating comprises statistical analysis.

7. (Canceled)

8. (Original) The method of claim 1, further comprising the step of producing hybridization profiles of said test and reference bacteria.

9. (Currently Amended) A method of identifying bacteria, comprising:

a) providing:

i) amplified random genomic DNA sequences from a plurality of bacterial reference species, wherein said amplified genomic DNA sequences range between 1 – 2 kb and are arrayed in a plurality of spots on a solid support so as to permit the sampling of 1-3% of each genome ~~on at least one microchip, so as to create a plurality of arrayed elements, and wherein the nucleotide sequence of said amplified genomic sequences comprises unknown sequences~~,

ii) labeled target DNA from a test bacteria of interest, wherein said labeled target DNA is labeled with a first fluorescent dye, and

iii) labeled reference DNA from at least four ~~strains~~ of said bacterial reference species ~~bacteria, wherein said reference bacteria are members of the group consisting of said plurality of bacterial species,~~ wherein said labeled target DNA is labeled with a second fluorescent dye,

b) hybridizing said target DNA and said reference DNA to said amplified genomic sequences ~~having unknown sequences on said plurality of arrayed elements~~, wherein each hybridized target DNA has a fluorescent target signal, and each hybridized reference DNA has a fluorescent reference signal, and

c) ~~determining the presence of 70% homology between said hybridized target DNA and one or more of said reference DNA by~~ comparing said fluorescent target signal with said fluorescent reference signal, and

d) identifying~~, without the need for sequencing said amplified genomic sequences,~~ the species of said test bacteria ~~based on said homology~~.

10. (Original) The method of claim 9, wherein said test bacteria are from a sample obtained from a subject.

11. (Previously Presented) The method of claim 10, wherein said test bacteria are pathogenic.

12. (Original) The method of claim 9, wherein said test bacteria are environmental isolates.

13. (Original) The method of claim 9, further comprising the step of producing hybridization profiles of said test and reference bacteria.

14. (Previously Presented) The method of claim 27, wherein said calculating comprises statistical analysis.

15-21. (Canceled)

22. (Currently Amended) The method of Claim 1, wherein said solid support comprises ~~at least~~ between 60 and 500,000 of said genomic sequences ~~arrayed elements~~.

23. (Currently Amended) The method of Claim 1, wherein said solid support comprises ~~at least~~ 96 of said genomic sequences ~~arrayed elements~~.

24. (Currently Amended) The method of Claim 9, wherein said solid support comprises ~~at least~~ between 60 and 500,000 of said genomic sequences ~~arrayed elements~~.

25. (Currently Amended) The method of Claim 9, wherein said solid support comprises ~~at least~~ 96 of said genomic sequences ~~arrayed elements~~.

26. (Currently Amended) The method of Claim 1, ~~further~~ wherein said comparing comprises~~ing~~ calculating a log ratio of said fluorescent target signal to said fluorescent reference signal ~~at each array element thereby determining the species of said test bacteria~~.

27. (Currently Amended) The method of Claim 9, ~~further~~ wherein said comparing comprises~~ing~~ calculating a log ratio of said fluorescent target signal to said fluorescent reference signal ~~at each array element thereby determining the species of said test bacteria~~.

28. (New) A method of identifying bacteria, comprising:

a) providing:

i) amplified random genomic DNA sequences from a plurality of bacterial reference species, wherein said amplified genomic DNA sequences range between 1 – 2 kb and are arrayed in a plurality of spots on a solid support so as to permit the sampling of 1-3% of each genome,

ii) labeled target DNA from a test bacteria of interest, wherein said labeled target DNA is labeled with a first fluorescent dye, and

iii) labeled reference DNA from at least four of said bacterial reference species wherein said labeled target DNA is labeled with a second fluorescent dye,

b) hybridizing said target DNA and said reference DNA to said amplified genomic sequences, wherein each hybridized target DNA has a fluorescent target signal, and each hybridized reference DNA has a fluorescent reference signal, and

c) determining an evenness value for each of said hybridized bacterial reference genomic sequences by comparing said fluorescent target signal with said fluorescent reference signal, and

d) identifying the species of said test bacteria when said hybridized bacterial reference genomic sequence evenness value is greater than 20°.